**Supplementary Data 1** | **Annotated HCD fragmentation spectrum.** Fragments were annotated using the "Interactive Peptide Spectral Annotator" web tool with 10 ppm mass accuracy. Spectra can be identified by raw file ("Sample") and scan number. Score refers to the Andromeda score. Fragment types are color coded: red (y), blue (b), green (c), purple (a), orange (z). Lower case letters represent modified amino acids: Deamidation (qn), Oxidation (m), Hydroxyproline (p), Arginine to Ornithine (r), and phosphorylation (s). Neutral losses were only annotated for water and ammonium, but not for phosphate losses.





























